

ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTTCTCGATACCGAAACCACCGGTATGAACCAGA 70
 M T A M S T A I T R Q I V L D T E T T G M N Q
 TTGTGCGCACTATGAAGGCCACAAGATCATTGAGATTGGTGCCTTGAAGTGGTGAACCGTCGCGCTGAC 140
 I G A H Y E G H K I I E I G A V E V V N R R L T
 GGGCAATAACTTCCATGTTTATCTCAAACCCGATCGGCTGGTGGATCCGGAAGCCTTTGGCGTACATGGT 210
 G N N F H V Y L K P D R L V D P E A F G V H G
 ATTGCCGATGAATTTTGTCTCGATAAGCCACGTTTGCCGAAGTAGCCGATGAGTTCATGGACTATATTC 280
 I A D E F L L D K P T F A E V A D E F M D Y I
 CGGCGCGGAGTTGGTGCATTAACGCAGCGTTTCGATATCGGCTTTATGGACTACGAGTTTCGTTGCT 350
 R G A E L V I H N A A F D I G F M D Y E F S L L
 TAAGCGCGATATTCGGAAGACCAATACTTTCTGTAAGGTACCCGATAGCCTTGCGGTGGCGAGGAAAAATG 420
 K R D I P K T N T F C K V T D S L A V A R K M
 TTTCCCGGTAAGCGCAACAGCCTCGATGCGTTATGTGCTCGCTACGAAATAGATAACAGTAAACGAACGC 490
 F P G K R N S L D A L C A R Y E I D N S K R T
 TGCACGGGGCATTACTCGATGCCAGATCCCTTGCGGAAGTTTATCTGGCGATGACGGGTGGTCAAACGTC 560
 L H G A L L D A Q I L A E V Y L A M T G G Q T S
 GATGGCTTTTGCATGGAAGGAGAGACACAACAGCAACAAGGTGAAGCAACAATTCAGCGCATTGTACGT 630
 M A F A M E G E T Q Q Q Q G E A T I Q R I V R
 CAGGCAAGTAAGTTACGCGTTGTTTTCGACAGATGAAGAGATTGCAGCTCATGAAGCCGCTCTCGATC 700
 Q A S K L R V V F A T D E E I A A H E A R L D
 TGGTGCAAGAAAGGCGGAAGTTGCCTCTGGCGAGCATAA 741
 L V Q K K G G S C L W R A .

FIGURE 1

10 20 30 40 50 60 70

10 ATGAGCTATCGATGTTGTTGATTTATCTGGTTCCTAAATGTGAACCTCTTGGCCCCGGCGCCGTTTCTGTTG Bb_429T.dna
 10 ATGAGCTATCGATGTTGTTGATTTATCTGGTTCCTAAATGTGAACCTCTTGGCCCCGGCGCCGTTTCTGTTG Bb_429T.dna

80 90 100 110 120 130 140

80 TTGGCCAGCGCTGCCAGCTGCTGGGGGGTAAAAAAGCCCTGCTGGTGACCCGATAAAGGCCCTGCGCGCCAT Bb_429T.dna
 80 TTGGCCAGCGCTGCCAGCTGCTGGGGGGTAAAAAAGCCCTGCTGGTGACCCGATAAAGGCCCTGCGCGCCAT Bb_429T.dna

150 160 170 180 190 200 210

150 AAAAGACGGTGCTGTCTGATCAGACCGTGAAGCACCCTGAAAGCCGCCGGTATTGAGGTGGTCAATTTCTGAC Bb_429T.dna
 150 TAAAGACGGTGCTGTCTGATCAGACCGTGAAGCACCCTGAAAGCCGCCGGTATTGAGGTGGTCAATTTCTGAC Bb_429T.dna

220 230 240 250 260 270 280

220 GGGGTCGAGCCGAACCCGAAAGACACCAACGTGCTCGACGGCCCTGGCCATGTTCCGTAAGAGCAGAGTGCG Bb_429T.dna
 220 GGGGTCGAGCCGAACCCGAAAGACACCAACGTGCTCGACGGCCCTGGCCATGTTCCGTAAGAGCAGAGTGCG Bb_429T.dna

290 300 310 320 330 340 350

290 ACATGATAATCACCGTCGGCGGGCGGCGAGCCCGCTGACTCGGGTAAAGGCATTGGTATTGCGGCCACCCA Bb_429T.dna
 290 ACATGATAATCACCGTCGGCGGGCGGCGAGCCCGCTGACTCGGGTAAAGGCATTGGTATTGCGGCCACCCA Bb_429T.dna

360 370 380 390 400 410 420

360 CCGGGGTGATCTGTACAGCTATGCGGGTATCGAAACACCTCAACCAACCGCTGCCGCCCATTTATGCGGGT Bb_429T.dna
 360 CCGGGGTGATCTGTACAGCTATGCGGGTATCGAAACACCTCAACCAACCGCTGCCGCCCATTTATGCGGGT Bb_429T.dna

430 440 450 460 470 480 490

430 AACCAACCCGCGCGGGAGCCGACGCAAGTCAACCGCCACTGCTGCTGACTAACCAACCAACCAAGATA Bb_429T.dna
 430 AACCAACCCGCGCGGGAGCCGACGCAAGTCAACCGCCACTGCTGCTGACTAACCAACCAACCAAGATA Bb_429T.dna

500 510 520 530 540 550 560

500 AATTTGTGATTGTGTCAGCTGGCGCAACCTGCTTCCGTCCTCCATTAAACGATCCGCTGCTGATGATCGGCA Bb_429T.dna
 500 AATTTGTGATTGTGTCAGCTGGCGCAACCTGCTTCCGTCCTCCATTAAACGATCCGCTGCTGATGATCGGCA Bb_429T.dna

570 580 590 600 610 620 630

570 GCGCGCGCGGCTGACCGCGCCACCGGATGGATGCGCTGACCCACCGCGGTAGAGGCCCTATATCTCCAAA Bb_429T.dna
 570 GCGCGCGCGGCTGACCGCGCCACCGGATGGATGCGCTGACCCACCGCGGTAGAGGCCCTATATCTCCAAA Bb_429T.dna

640 650 660 670 680 690 700

640 GACGCCAACCCGGTTACCGATGCTCTGCTATTACAGGCCATCAAACTGATTGCCACCAACTTGCGCCAGG Bb_429T.dna
 640 GACGCCAACCCGGTTACCGATGCTCTGCTATTACAGGCCATCAAACTGATTGCCACCAACTTGCGCCAGG Bb_429T.dna

710 720 730 740 750 760 770

710 CCGTCGCCCTGGGGACCAACCTCAAAAGCCGTGAAAAACATGGCCCTGCGCCTCTCTGCTGCCCGGGATGGC Bb_429T.dna
 710 CCGTCGCCCTGGGGACCAACCTCAAAAGCCGTGAAAAACATGGCCCTGCGCCTCTCTGCTGCCCGGGATGGC Bb_429T.dna

780 790 800 810 820 830 840

780 CTTTAAACAACGCCAACCTGGGCTATGTTACAGCCATGGCTACCAAGCTGGCGGCGCTGTACGACATGGCC Bb_429T.dna
 780 CTTTAAACAACGCCAACCTGGGCTATGTTACAGCCATGGCTACCAAGCTGGCGGCGCTGTACGACATGGCC Bb_429T.dna

850 860 870 880 890 900 910

850 CACGGGGTGGCGAACCGGCTCTGCTGCCCTATGCTGCCCTATAAAGCTGATTGCCCAACCCGGAATAA Bb_429T.dna
 850 CACGGGGTGGCGAACCGGCTCTGCTGCCCTATGCTGCCCTATAAAGCTGATTGCCCAACCCGGAATAA Bb_429T.dna

920 930 940 950 960 970 980

920 TTGCGGATATGCCACCTTTATGGGGGAAAAACACACCGGCTTTTCACCATGGACGACGCGGAGCTGGC Bb_429T.dna
 920 TTGCGGATATGCCACCTTTATGGGGGAAAAACACACCGGCTTTTCACCATGGACGACGCGGAGCTGGC Bb_429T.dna

990 1000 1010 1020 1030 1040 1050

990 CATCAGCGCCATTGCCCGCTGCTTAAAGATGTCGGGATCCCGACGACCTGCGTGAACTGGGGGTAATA Bb_429T.dna
 990 CATCAGCGCCATTGCCCGCTGCTTAAAGATGTCGGGATCCCGACGACCTGCGTGAACTGGGGGTAATA Bb_429T.dna

1060 1070 1080 1090 1100 1110 1120

1060 GAGGCGCACTTCCCGTACATGGCAGAAATGCCCTGAAAGACGGCAACGCCCTTCTCTAAACCCGCGCAAG Bb_429T.dna
 1060 GAGGCGCACTTCCCGTACATGGCAGAAATGCCCTGAAAGACGGCAACGCCCTTCTCTAAACCCGCGCAAG Bb_429T.dna

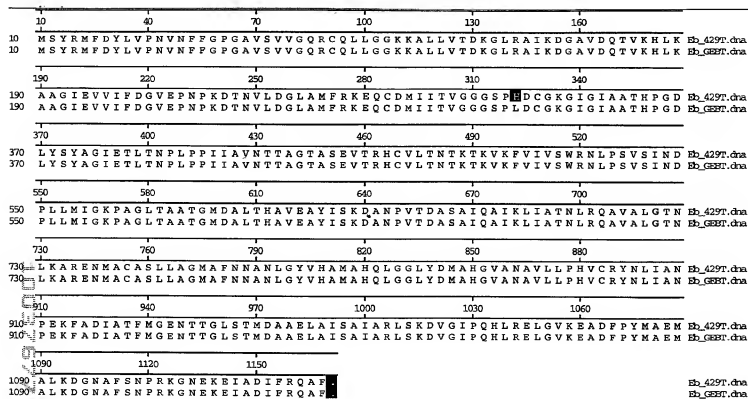
1130 1140 1150 1160 1170

1130 GGAACGAAAAAGAGATTGCCGACATTTTCCGCCAGGCAATTCGTA Bb_429T.dna
 1130 GGAACGAAAAAGAGATTGCCGACATTTTCCGCCAGGCAATTCGTA Bb_429T.dna

FIGURE 2

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

Bb_429T.dna
 Bb_429T.dna



Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIGURE 3

10037677.102301

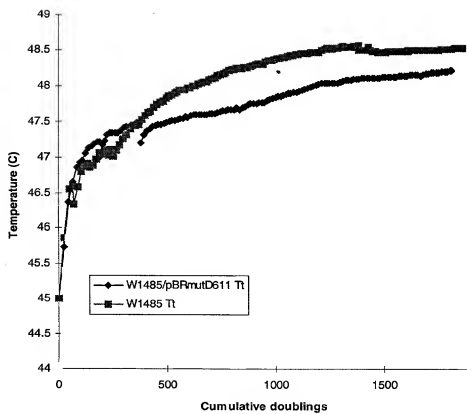


Figure 4

E. blattae 33429 pH 7
Glycerol fermentation

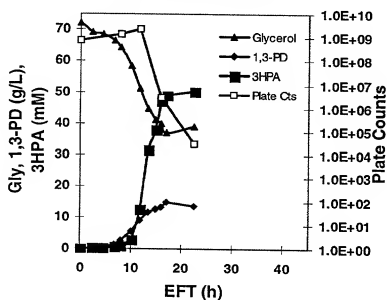


Figure 5

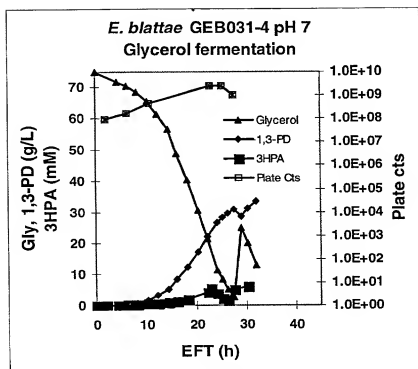


Figure 6